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<110> Schnoor, Kirk  
Jorgensen, Lina  
Schulein, Martin

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Lys Glu Leu Val Asp Arg Ser Val Ser Leu Ser Lys Ala Ala Lys Ala  
245 250 255

Val Asp Ala Gly Ala Glu Ile Phe Gly Pro Val Leu Tyr Gly Phe Gly  
260 265 270

Ala Tyr Lys Asp Leu Gln Thr Ala Pro Asp Trp Asn Ser Val Lys Gly  
275 280 285

Asn Tyr Ser Trp Phe Val Asp Tyr Tyr Leu Asp Gln Met Arg Leu Ser  
290 295 300

Ser Gln Ala Glu Gly Lys Arg Leu Leu Asp Val Phe Asp Val His Trp  
305 310 315 320

Tyr Pro Glu Ala Met Gly Gly Gly Ile Arg Ile Thr Asn Glu Val Gly  
325 330 335

Asn Asp Glu Thr Lys Lys Ala Arg Met Gln Ala Pro Arg Thr Leu Trp  
340 345 350

Asp Pro Thr Tyr Lys Glu Asp Ser Trp Ile Ala Gln Trp Asn Ser Glu  
355 360 365

Phe Leu Pro Leu Leu Pro Arg Leu Lys Gln Ser Val Asp Lys Tyr Tyr  
370 375 380

Pro Gly Thr Lys Leu Ala Leu Thr Glu Tyr Ser Tyr Gly Gly Glu Asn  
 385 390 395 400

Asp Ile Ser Gly Gly Ile Ala Met Ala Asp Val Leu Gly Ile Leu Gly  
 405 410 415

Lys Asn Asp Val Tyr Met Ala Asn Tyr Trp Lys Leu Lys Asp Gly Ala  
 420 425 430

Asn Asn Tyr Val Ser Ala Ala Tyr Lys Leu Tyr Arg Asn Tyr Asp Gly  
 435 440 445

Lys Ser Ser Thr Phe Gly Asp Ile Ser Val His Ala Gln Thr Ser Asp  
 450 455 460

Ile Val Asn Ser Ser Val His Ala Ser Val Thr Asp Ala Ser Tyr Lys  
 465 470 475 480

Glu Leu His Leu Val Val Met Asn Lys Ser Met Asp Ser Ala Phe Asp  
 485 490 495

Ala Gln Phe Asp Leu Ser Gly Glu Thr Thr Tyr Gly Ser Gly Lys Val  
 500 505 510

Trp Gly Phe Asp Lys Asn Ser Ser Gln Ile Lys Glu Ala Ala Pro Ile  
 515 520 525

Thr Gln Ile Ser Gly Asn Arg Phe Thr Tyr Thr Val Pro Pro Leu Thr  
 530 535 540

Ala Tyr His Ile Val Leu Thr Ala Gly Asn Asp Thr Pro Val Glu Asn  
 545 550 555 560

Pro Glu Ser Phe Ala Leu Arg Ala Glu Ala Gly Asp Gly Lys Ser Ile  
 565 570 575

Tyr Leu Asp Ala Ser Ser Gly Val Val Gly Tyr Ser Val Gln Arg Ala  
 580 585 590

Thr Tyr Glu Asn Gly Pro Phe Ala Ala Val Ala Ser Asn Leu Val Glu  
 595 600 605

Thr Ser Tyr Thr Asp Thr Asn Val Thr Asn Gly Thr Ser Tyr Tyr Tyr  
 610 615 620

Lys Ile Thr Ala Lys Thr Lys Thr Gly Thr Ser Ala Ser Asn Val Leu  
625 630 635 640

Lys Ala Val Pro Arg Ala Pro Val Asp Gly Pro Asp Arg Tyr Glu Ala  
645 650 655

Glu Asp Gly Thr Leu Lys Gly Thr Val Val Glu Ser Ser Gly Thr Gly  
660 665 670

Phe Ser Gly Thr Gly Tyr Val Thr Asn Phe His Asn Ala Gly Asp Ser  
675 680 685

Leu Thr Met Thr Ile Gln Ala Pro Thr Ala Gly Leu Tyr Asn Leu Thr  
690 695 700

Ile Gly Tyr Arg Ser Pro His Asp Asp Lys Arg Thr Asn Phe Ser Leu  
705 710 715 720

Asn Gly Lys Ala Ser Gly Glu Leu Val Leu Trp Lys Thr Ala Asp Phe  
725 730 735

Lys Glu Thr Ser Gly Gly Lys Val Leu Leu Asn Ala Gly Ala Asn Thr  
740 745 750

Ile Gly Phe Glu Thr Gly Trp Gly Trp Tyr Asp Ile Asp Tyr Val Lys  
755 760 765

Leu Glu Pro Ala Ala Asp Arg Pro Pro His Ala Val Thr Lys Thr Leu  
770 775 780

Ile Asn Pro Asn Ala Thr Val Glu Ala Lys Ala Leu Met Asn Tyr Leu  
785 790 795 800

Val Asp Gln Tyr Gly Lys Asn Met Leu Ser Gly Gln Glu Asp Met Pro  
805 810 815

Glu Ile Asp Trp Leu Gln Ala Asn Val Gly Lys Lys Pro Ala Ile Ala  
820 825 830

Ala Leu Asp Leu Ile Asp Tyr Ser Pro Ser Arg Ala Glu His Gly Leu  
835 840 845

Ser Ser Thr Glu Thr Glu Lys Ala Ile Glu Trp Asp Lys Gln Gly Gly  
850 855 860

Ile Val Thr Phe Ala Trp His Trp Asn Ala Pro Lys Gly Leu Ile Asp  
865 870 875 880

Thr Gln Gly Lys Glu Trp Trp Arg Gly Phe Tyr Ala Asp Ser Thr Thr  
885 890 895

Phe Asp Ile Glu Tyr Ala Met Asn His Pro Glu Ser Glu Asp Tyr Lys  
900 905 910

Leu Leu Ile Arg Asp Ile Asp Val Ile Ala Gly Gln Leu Lys Lys Leu  
915 920 925

Gln Asp Ala Lys Val Pro Val Leu Phe Arg Pro Leu His Glu Ala Glu  
930 935 940

Gly Lys Trp Phe Trp Trp Gly Ala Lys Gly Pro Glu Pro Val Lys Lys  
945 950 955 960

Leu Tyr Ile Leu Met His Asp Arg Leu Thr Asn Val His Lys Leu Asn  
965 970 975

Asn Leu Ile Trp Val Trp Asn Ser Val Ala Pro Asp Trp Tyr Pro Gly  
980 985 990

Asp Glu Tyr Val Asp Ile Leu Ser Phe Asp Ser Tyr Pro Gln Ala Gly  
995 1000 1005

Asp Tyr Ser Pro Gln Ile Ala Lys Tyr Glu Asp Leu Val Thr Leu  
1010 1015 1020

Gly Lys Asp Lys Lys Leu Val Cys His Glu Arg Lys Arg Thr Tyr  
1025 1030 1035

Pro Gly Pro Gly Ser Asp Glu Gly Val Ser Ser Pro Leu Glu Leu  
1040 1045 1050

Val Arg Tyr Met Val Trp Gly Phe Leu Glu Arg Arg Gln Thr Lys  
1055 1060 1065

Gln Ser Leu Glu His Leu Lys Lys Val Tyr Asn His Pro Asn Val  
1070 1075 1080



Ile Thr Leu Glu Lys Leu Pro Thr Asn Leu Lys Thr Tyr Gly Ile  
 1085 1090 1095

Thr Glu Gln Pro Ser Val Pro Gly Ser Phe Thr Leu Asn Ala Ala  
 1100 1110

Gly Glu Thr Ala Lys Val Lys Leu Ser Trp Thr Ala Ser Ala Asn  
 1115 1120 1125

Ala Ala Ser Tyr Glu Val Lys Arg Ser Thr Val Glu Asn Gly Ala  
 1130 1135 1140

Phe Ala Thr Val Ala Ser Asp Val Tyr Gly Ser Ser Tyr Thr Asp  
 1145 1150 1155

Thr Ala Val Thr Ala Asp Thr Thr Tyr Tyr Tyr Gln Val Val Ala  
 1160 1165 1170

Lys Asn Asp Ala Gly Gln Thr Val Ser Asn Thr Ala Ser Ala Ala  
 1175 1180 1185

Pro Lys Ala Asp Thr Gln Gln Pro Thr Thr Gly Leu Val Leu Gln  
 1190 1195 1200

Tyr Arg Thr Ala Asp Thr Asn Val Asn Asp Asn His Leu Asn Pro  
 1205 1210 1215

His Phe Gln Ile Leu Asn Lys Gly Thr Ile Ser Val Pro Ile Asn  
 1220 1225 1230

Glu Leu Lys Ile Arg Tyr Tyr Tyr Thr Ile Asp Gly Asp Arg Glu  
 1235 1240 1245

Gln Thr Phe Asn Cys Asp Tyr Ala Val Leu Ser Cys Ser Lys Leu  
 1250 1255 1260

Asn Gly Lys Leu Val Lys Met Asp Lys Ala Ala Thr Gly Ala Asp  
 1265 1270 1275

Tyr Tyr Leu Glu Val Ser Phe Asn Ser Asp Ala Gly Val Leu Ala  
 1280 1285 1290

Ser Gly Gly Ser Thr Gly Gly Ile Gln Thr Arg Ile His Lys Ala  
 1295 1300 1305

Asp Trp Ser Asn Tyr Asn Glu Ser Asp Asp Tyr Ser Tyr Lys Gly  
 1310 1315 1320

Thr Gln Thr Ser Phe Asp Asp His Thr Lys Ala Thr Leu Tyr His  
 1325 1330 1335

Asn Gly Val Leu Val Trp Gly Thr Glu Thr Ala Asn  
 1340 1345 1350

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 <211> 2141  
 <212> DNA  
 <213> Paenibacillus pabuli

<220>  
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 <222> (1)..(2141)  
 <223> n is unknown nucleotide

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 acggcaaaga ccgttaccat taaagtcgat acatccaagg atcgtaagcc tattagtcct 180  
 tatatatacg gtacgaatca ggatttggca ggcgatgaaa atctggctgc cagacgactt 240  
 ggtggcaatc gaatgaccgg atacaactgg gaaaataata tgtccaatgc gggaagcgat 300  
 tggcagcaat ctagcgataa ctttttatgc aacaatgggt gcctgacaaa agccgaatgt 360  
 gaaaagccgg gagcagtgac gacttcgttt catgatcaat cgctgaagct gggcgcttat 420  
 tcttttagtca cgctgccgat ggccggttat gtggccaagg atggaaacgg aagtgtgcag 480  
 gaaagcgaac aggtccttc cgctcgttgg aatcaggctg taaatgccaa aaatgcgccg 540  
 ttccaactac agcctgatct gaatgacaat caggtatatg cggatgaatt cgtcaatttt 600  
 ttagtgaaaa agtacggcgc tgcttcaaca aaggcgggtg tgaaaggata tgcgctcgac 660  
 aatgaaccgg ctctctggtc gcatacgcat ccgcgcattc atggtgaaaa agtcnnnnnn 720  
 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 780  
 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnttcaaact gcacntgatt 840  
 ggaacttctg taaaaggcaa ctatagctgg ttcgtggact attacctgga tcaaatgcgc 900

ctcaactcgc aagccgaagg caagagattg ctggatgtat tcgatgtgca ctggtatccc 960  
 gaagcgatgg gcggagggcat acgaattaca aatgaggtag gcaatgacga aacgaagaaa 1020  
 gccagaatgc aggcgcctcg tactttgtgg gacccgacct acaaggaaga tagctggatc 1080  
 gctcaatgga acagcgcatt ctgaccttta ctgcctcgat tgaagcagtc ggtggacaag 1140  
 tattacccgg gaaccaagct ggctttgacc gagtatagct acggcggcga aaatgatatt 1200  
 tccggcggta ttgctatgac cgatgtgctg ggcatcttgg gcaaaaacga cgtttatatg 1260  
 gcgaactatt ggaagttaaa ggatgggtgcc aacaactacg ttagcgccgc ttacaagctt 1320  
 taccgcaatt atgacggaaa aaacgctact ttcggcgata tcagcgtaa tgcgcaaacg 1380  
 tcggatattg ttaatagctc ggtgcatgct tccgtaacgg atgcatccta caaagaactg 1440  
 cacctcattg tcatgaataa aagcatggac agcgcattcg acgccaatt cgatctttcc 1500  
 ggcgagacga cttacagtcc cggtaaaata tggggcttcg ataaaaatag ctcgcaaatt 1560  
 aaggcagtag cgccaatcac gcaaatttca ggcaaccgct ttacctatac agtaccacct 1620  
 ttgacggctt atcacatcgt gttgactgcc gacaatgata cacctgtgcc acctgtggaa 1680  
 gatcctgaaa gctttacgct gagggctgag gctggcgatg ggaaagtcga tttgtcctgg 1740  
 gacgcttcca gcggagtgtt ggggttacagt gtacagcggg caacgtatga aaacggtcct 1800  
 tttgtgtctg tagcatccaa cttgggtcgaa acgtcttata cggatacgaa cgtaacgaac 1860  
 ggcacttctt actattataa aataaccgca aaaacaaagg cgggaacgag cgaatccaat 1920  
 gtcttgaaag cggttccgcg aacgcctgta gacggcccg atcgctatga agccgaagat 1980  
 ggcacgctga agggaaccat tgtggaatcc agcgggaccg gcttctccgg tactggttat 2040  
 gtaactaatt tccacaatgc aggggattcc ctgacgatga cgatccacta gtgtcgacct 2100  
 gcaggcgcgc gagctccagc tttgttccc tttagtgagg g 2141

<210> 6  
 <211> 695  
 <212> PRT  
 <213> Paenibacillus pabuli

<220>  
 <221> MISC\_FEATURE  
 <222> (1)..(695)  
 <223> Xaa is an unknown amino acid

<400> 6

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Ala Pro Thr Val Val His Gly Gln Thr Ala Lys Thr Val Thr Ile Lys  
35 40 45

Val Asp Thr Ser Lys Asp Arg Lys Pro Ile Ser Pro Tyr Ile Tyr Gly  
50 55 60

Thr Asn Gln Asp Leu Ala Gly Asp Glu Asn Leu Ala Ala Arg Arg Leu  
65 70 75 80

Gly Gly Asn Arg Met Thr Gly Tyr Asn Trp Glu Asn Asn Met Ser Asn  
85 90 95

Ala Gly Ser Asp Trp Gln Gln Ser Ser Asp Asn Phe Leu Cys Asn Asn  
100 105 110

Gly Gly Leu Thr Lys Ala Glu Cys Glu Lys Pro Gly Ala Val Thr Thr  
115 120 125

Ser Phe His Asp Gln Ser Leu Lys Leu Gly Ala Tyr Ser Leu Val Thr  
130 135 140

Leu Pro Met Ala Gly Tyr Val Ala Lys Asp Gly Asn Gly Ser Val Gln  
145 150 155 160

Glu Ser Glu Gln Ala Pro Ser Ala Arg Trp Asn Gln Val Val Asn Ala  
165 170 175

Lys Asn Ala Pro Phe Gln Leu Gln Pro Asp Leu Asn Asp Asn Gln Val  
180 185 190

Tyr Ala Asp Glu Phe Val Asn Phe Leu Val Lys Lys Tyr Gly Ala Ala  
195 200 205

Ser Thr Lys Ala Gly Val Lys Gly Tyr Ala Leu Asp Asn Glu Pro Ala  
210 215 220

Leu Trp Ser His Thr His Pro Arg Ile His Gly Glu Lys Val Xaa Xaa  
225 230 235 240

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
245 250 255

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
260 265 270

Xaa Xaa Phe Lys Leu His Xaa Ile Gly Thr Ser Val Lys Gly Asn Tyr  
275 280 285

Ser Trp Phe Val Asp Tyr Tyr Leu Asp Gln Met Arg Leu Asn Ser Gln  
290 295 300

Ala Glu Gly Lys Arg Leu Leu Asp Val Phe Asp Val His Trp Tyr Pro  
305 310 315 320

Glu Ala Met Gly Gly Gly Ile Arg Ile Thr Asn Glu Val Gly Asn Asp  
325 330 335

Glu Thr Lys Lys Ala Arg Met Gln Ala Pro Arg Thr Leu Trp Asp Pro  
340 345 350

Thr Tyr Lys Glu Asp Ser Trp Ile Ala Gln Trp Asn Ser Ala Phe Leu  
355 360 365

Pro Leu Leu Pro Arg Leu Lys Gln Ser Val Asp Lys Tyr Tyr Pro Gly  
370 375 380

Thr Lys Leu Ala Leu Thr Glu Tyr Ser Tyr Gly Gly Glu Asn Asp Ile  
385 390 395 400

Ser Gly Gly Ile Ala Met Thr Asp Val Leu Gly Ile Leu Gly Lys Asn  
405 410 415

Asp Val Tyr Met Ala Asn Tyr Trp Lys Leu Lys Asp Gly Ala Asn Asn  
420 425 430

Tyr Val Ser Ala Ala Tyr Lys Leu Tyr Arg Asn Tyr Asp Gly Lys Asn  
435 440 445

Ala Thr Phe Gly Asp Ile Ser Val Asn Ala Gln Thr Ser Asp Ile Val  
450 455 460

Asn Ser Ser Val His Ala Ser Val Thr Asp Ala Ser Tyr Lys Glu Leu  
465 470 475 480

His Leu Ile Val Met Asn Lys Ser Met Asp Ser Ala Phe Asp Ala Gln  
485 490 495

Phe Asp Leu Ser Gly Glu Thr Thr Tyr Ser Ser Gly Lys Ile Trp Gly  
500 505 510

Phe Asp Lys Asn Ser Ser Gln Ile Lys Ala Val Ala Pro Ile Thr Gln  
515 520 525

Ile Ser Gly Asn Arg Phe Thr Tyr Thr Val Pro Pro Leu Thr Ala Tyr  
530 535 540

His Ile Val Leu Thr Ala Asp Asn Asp Thr Pro Val Pro Pro Val Glu  
545 550 555 560

Asp Pro Glu Ser Phe Thr Leu Arg Ala Glu Ala Gly Asp Gly Lys Val  
565 570 575

Asp Leu Ser Trp Asp Ala Ser Ser Gly Val Val Gly Tyr Ser Val Gln  
580 585 590

Arg Ala Thr Tyr Glu Asn Gly Pro Phe Ala Ala Val Ala Ser Asn Leu  
595 600 605

Val Glu Thr Ser Tyr Thr Asp Thr Asn Val Thr Asn Gly Thr Ser Tyr  
610 615 620

Tyr Tyr Lys Ile Thr Ala Lys Thr Lys Ala Gly Thr Ser Glu Ser Asn  
625 630 635 640

Val Leu Lys Ala Val Pro Arg Thr Pro Val Asp Gly Pro Asp Arg Tyr  
645 650 655

Glu Ala Glu Asp Gly Thr Leu Lys Gly Thr Ile Val Glu Ser Ser Gly  
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Thr Gly Phe Ser Gly Thr Gly Tyr Val Thr Asn Phe His Asn Ala Gly  
675 680 685

Asp Ser Leu Thr Met Thr Ile  
690 695

<210> 7  
<211> 42  
<212> DNA  
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42

<210> 8  
<211> 64  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Primer

<400> 8  
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64

agat

<210> 9  
<211> 61  
<212> DNA  
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<220>  
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<400> 9  
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61

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<210> 10  
<211> 35  
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35

<210> 11  
<211> 35  
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<220>

<223> Primer

<400> 11  
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35

<210> 12  
<211> 37  
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<223> Primer

<400> 12  
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37

<210> 13  
<211> 83  
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<220>  
<223> Primer

<400> 13  
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60

83

<210> 14  
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<212> DNA  
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<220>  
<223> Primer

<400> 14  
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25

<210> 15  
<211> 39  
<212> DNA  
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<220>  
<223> Primer

<400> 15  
gcattctgca gcagcggtg tggttcacgg tcaaacggc

39

<210> 16  
<211> 40



<212> DNA  
<213> Artificial sequence

<220>  
<223> Primer

<400> 16  
gctaggcgcg cctacactgg agacgtgtca ttgccagtag

40